AMENDMENTS TO THE CLAIMS

Please amend Claims 17, 18 and 20 and add new Claims 25-37 as indicated below.

1-16. **(Canceled)**

17. **(Currently amended)** A diagnostic ~~hearing loss~~ microarray comprising ~~at least 5~~ nucleic acid sequences, wherein said sequences comprise a set of hearing loss sequences that are indicative of presence or absence of an allele associated with a risk for hearing loss, and wherein said ~~sequences are selected from the group consisting of~~ set consists essentially of genetic sequences ~~from~~ found in CDH23, MYO7A, OTOF, SLC26A4 and USH2A genes.

18. **(Currently amended)** The microarray of Claim 17, wherein said ~~sequences comprise~~ set comprises sequences found in multiple adjacent exons.

19. **(Previously Presented)** The microarray of Claim 18, wherein said multiple adjacent exons are selected from the group comprising CDH23 exons 2-3, CDH23 exons 4-6, CDH23 exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4 exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

20. **(Currently amended)** The microarray of Claim 17, wherein said ~~sequences comprise~~ set comprises sequences found in a single exon.

21. **(Previously Presented)** The microarray of Claim 20, wherein said single exon is selected from the group consisting of MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.

22. **(Original)** A kit for detecting a candidate gene responsible for hearing loss comprising:

a microarray of Claim 17; and

buffers and components to be used with said microarray.

23. **(Original)** The kit of Claim 22, wherein the microarray comprises a solid support comprising a plurality of capture nucleotide sequences bound to the solid support, wherein said capture nucleotide sequences are representative of regions of candidate genes for hearing loss, and wherein the support of the kit is adapted to be contacted with a sample from a patient comprising target nucleic acid sequences, and wherein the contacting permits hybridization under stringent conditions of a target nucleic acid sequence and a capture nucleotide sequence representative of regions of candidate genes for hearing loss.

24. **(Canceled)**

25. **(New)** The microarray of Claim 17, wherein said set consists of genetic sequences found in CDH23, MYO7A, OTOF, SLC26A4 and USH2A genes.

26. **(New)** A microarray comprising a plurality of nucleic acid molecules for analysis, wherein said nucleic acid molecules include a set of probes for allelic variants of hearing loss genes, and wherein said set consists essentially of probes for allelic variants of CDH23, MYO7A, OTOF, SLC26A4 and USH2A genes.

27. **(New)** The microarray of Claim 26, wherein said nucleic acid molecules comprise oligonucleotide probes.

28. **(New)** The microarray of Claim 27, wherein said oligonucleotide probes are 20-25 nucleotides in length.

29 **(New)** The microarray of Claim 26, wherein said plurality of nucleic acid molecules are bound to a solid support.

30. **(New)** The microarray of Claim 26, wherein said set comprises probes for a plurality of allelic variants for each of said CDH23, MYO7A, OTOF, SLC26A4 and USH2A genes.

31. **(New)** The microarray of Claim 26, wherein said microarray comprises perfect match and mismatches of said allelic variants.

32. **(New)** The microarray of Claim 26, wherein said allelic variants comprise a deletion mutant.

33. **(New)** The microarray of Claim 26, wherein said set consists of probes for allelic variants of CDH23, MYO7A, OTOF, SLC26A4 and USH2A genes.

34. **(New)** The microarray of Claim 26, wherein said set comprises sequences found in multiple adjacent exons.

35. **(New)** The microarray of Claim 34, wherein said multiple adjacent exons are selected from the group comprising CDH23 exons 2-3, CDH23 exons 4-6, CDH23 exons 7-9, CDH23 exons 10-11, CDH23 exons 12-13, CDH23 exons 14-16, CDH23 exons 17-21, CDH23 exons 22-27, CDH23 exons 28-31, CDH23 exons 32-36, CDH23 exons 37-43, CDH23 exons 44-46, CDH23 exons 47-53, CDH23 exons 53-68, MYO7A exons 5-14, MYO7A exons 16-21, MYO7A exons 16-18, MYO7A exons 22-26, MYO7A exons 28-35, MYO7A exons 36-44, MYO7A exons 45-49, OTOF exons 4-5, OTOF exons 6-8, OTOF exons 9-11, OTOF exons 12-25, OTOF exons 16-25, OTOF exons 16-18, OTOF exons 16-20, OTOF exons 19-20, OTOF exons 21-25, OTOF exons 16-39, OTOF exons 26-39, OTOF exons 40-47, SLC26A4 exons 1-3, SLC26A4 exons 4-6, SLC26A4 exons 11-18, SLC26A4 exons 19-21, USH2A exons 1-3, USH2A exons 5-9, USH2A exons 10-11, USH2A exons 12-13, USH2A exons 15-16 and USH2A exons 17-20.

36. **(New)** The microarray of Claim 26, wherein said set comprises sequences found in a single exon.

37. **(New)** The microarray of Claim 36, wherein said single exon is selected from the group consisting of MYO7A exon 1, MYO7A exon 2, MYO7A exon 3, MYO7A exon 4, MYO7A exon 15, MYO7A exon 21, MYO7A exon 27, OTOF exon 1, OTOF exon 2, OTOF exon 3, USH2A exon 4, USH2A exon 14 and USH2A exon 21.